

SCORE Search Results Details for Application 10667966 and Search Result us-10-667-966b-9.rag.

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This page gives you Search Results detail for the Application 10667966 and Search Result us-10-667-966b-9.rag.

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OM protein - protein search, using sw model

Run on: September 28, 2006, 04:38:19 ; Search time 104.18 Seconds
(without alignments)
197.493 Million cell updates/sec

Title: US-10-667-966B-9
Perfect score: 239
Sequence: 1 SLEQIWNNMTWEEWDREINN.....HELIEESQNQQEKNEQELLX 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1	239	100.0	44	8	ADO44125	Ado44125	Amino aci
2	239	100.0	45	8	ADO44133	Ado44133	Amino aci
3	233	97.5	44	8	ADO44132	Ado44132	Amino aci
4	222	92.9	51	9	AEB96643	Aeb96643	HIV gp41
5	222	92.9	52	9	AEB96642	Aeb96642	HIV gp41
6	222	92.9	53	9	AEB96641	Aeb96641	HIV gp41
7	222	92.9	54	9	AEB96640	Aeb96640	HIV gp41
8	222	92.9	55	9	AEB96639	Aeb96639	HIV gp41
9	222	92.9	56	9	AEB96638	Aeb96638	HIV gp41
10	222	92.9	57	5	AAO18796	Aao18796	HIV gp41
11	222	92.9	57	9	ADY71517	Ady71517	HIV-1 tra
12	222	92.9	57	9	AEB96637	Aeb96637	HIV gp41
13	222	92.9	58	4	AAU14128	Aau14128	DP178-lik
14	222	92.9	58	9	AEB96636	Aeb96636	HIV gp41
15	222	92.9	59	9	AEB96635	Aeb96635	HIV gp41
16	222	92.9	60	9	AEB96634	Aeb96634	HIV gp41
17	222	92.9	61	9	AEB96633	Aeb96633	HIV gp41
18	222	92.9	62	9	AEB96632	Aeb96632	HIV gp41
19	222	92.9	63	9	AEB96631	Aeb96631	HIV gp41
20	222	92.9	64	8	ADN06887	Adn06887	Human imm
21	222	92.9	64	8	ADS87222	Ads87222	HIV-1 gp4
22	222	92.9	64	9	AEB32178	Aeb32178	HIV glyco
23	222	92.9	64	9	AEB96630	Aeb96630	HIV gp41
24	222	92.9	64	9	AED69064	Aed69064	HIV gp41
25	222	92.9	65	9	AEB96629	Aeb96629	HIV gp41
26	222	92.9	66	9	AEB96628	Aeb96628	HIV gp41
27	222	92.9	66	9	AEB96670	Aeb96670	HIV gp41
28	222	92.9	67	9	AEB96627	Aeb96627	HIV gp41
29	222	92.9	67	9	AEB96669	Aeb96669	HIV gp41
30	222	92.9	68	9	AEB96668	Aeb96668	HIV gp41
31	222	92.9	69	9	AEB96626	Aeb96626	HIV gp41
32	222	92.9	69	9	AEB96667	Aeb96667	HIV gp41
33	222	92.9	70	9	AEB96625	Aeb96625	HIV gp41
34	222	92.9	70	9	AEB96666	Aeb96666	HIV gp41
35	222	92.9	71	9	AEB96665	Aeb96665	HIV gp41
36	222	92.9	71	9	AEB96624	Aeb96624	HIV gp41
37	222	92.9	72	9	AEB96664	Aeb96664	HIV gp41
38	222	92.9	72	9	AEB96623	Aeb96623	HIV gp41
39	222	92.9	73	9	AEB96554	Aeb96554	HIV gp41
40	222	92.9	73	9	AEB96549	Aeb96549	HIV gp41
41	222	92.9	73	9	AEB96622	Aeb96622	HIV gp41
42	222	92.9	114	2	AAR77185	Aar77185	Chimeric
43	222	92.9	138	3	AAY69792	Aay69792	HIV-1 gp4
44	222	92.9	138	8	ADO10354	Ado10354	HIV1 glyc
45	222	92.9	140	1	AAP93342	Aap93342	HIV-1 env

ALIGNMENTS

RESULT 1

ADO44125

ID ADO44125 standard; peptide; 44 AA.

XX

AC ADO44125;

XX

DT 15-JUL-2004 (first entry)

XX

DE Amino acid sequence of HIV variant gp41 peptide FB005.

XX

KW gp41; HIV; antiviral; virostatic; antifusogenic; viral infection.

XX

OS Human immunodeficiency virus.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

SCORE Search Results Details for Application 10667966 and Search Result us-10-667-966b-10.rag.

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This page gives you Search Results detail for the Application 10667966 and Search Result us-10-667-966b-10.rag.

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OM protein - protein search, using sw model

Run on: September 28, 2006, 04:38:19 ; Search time 78.7135 Seconds
(without alignments)
197.493 Million cell updates/sec

Title: US-10-667-966B-10
Perfect score: 185
Sequence: 1 WEEWDREINNYTXLIHELIEESQNQQEKNEWELL 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1	184	99.5	34	8	ADO44134	Ado44134	Amino aci
2	173	93.5	44	5	ADE02492	Ade02492	Hybrid po
3	171	92.4	34	8	ADO44126	Ado44126	Amino aci
4	171	92.4	35	8	ADO44135	Ado44135	Amino aci
5	171	92.4	44	8	ADO44132	Ado44132	Amino aci
6	171	92.4	44	8	ADO44125	Ado44125	Amino aci
7	171	92.4	45	8	ADO44133	Ado44133	Amino aci
8	167	90.3	34	8	ADO44131	Ado44131	Amino aci
9	167	90.3	34	8	ADO44138	Ado44138	Amino aci
10	167	90.3	35	8	ADO44139	Ado44139	Amino aci
11	162	87.6	35	8	ADT76688	Adt76688	Antiviral
12	162	87.6	35	8	ADT76692	Adt76692	Antiviral
13	162	87.6	36	4	ABB02297	Abb02297	Viral cor
14	162	87.6	36	4	ABB02285	Abb02285	Viral cor
15	161	87.0	34	6	ABR58073	Abr58073	HIV gp41
16	161	87.0	34	8	ADU66496	Adu66496	HIV-1 gp4
17	161	87.0	36	3	AAY89415	Aay89415	Core poly
18	161	87.0	36	3	AAY89401	Aay89401	Core poly
19	161	87.0	36	4	AAB77816	Aab77816	Core poly
20	161	87.0	36	4	AAU13369	Aau13369	DP178-lik
21	161	87.0	36	4	AAU13355	Aau13355	DP178-lik
22	161	87.0	344	8	ADR19628	Adr19628	Human imm
23	160	86.5	34	3	AAY89397	Aay89397	Core poly
24	160	86.5	34	3	AAY76979	Aay76979	HIV-1 gp4
25	160	86.5	34	3	AAB14534	Aab14534	HIV-1 iso
26	160	86.5	34	4	AAG63862	Aag63862	Amino aci
27	160	86.5	34	4	AAB85202	Aab85202	HIV gp41
28	160	86.5	34	4	AAB85203	Aab85203	HIV HXB3
29	160	86.5	34	4	AAB77798	Aab77798	Core poly
30	160	86.5	34	4	AAU70194	Aau70194	HIV viral
31	160	86.5	34	4	AAB99722	Aab99722	HIV-1 LAI
32	160	86.5	34	4	ABB00805	Abb00805	Viral DP1
33	160	86.5	34	4	ABB02281	Abb02281	Viral cor
34	160	86.5	34	4	AAB49501	Aab49501	C34 pepti
35	160	86.5	34	4	AAU13351	Aau13351	DP178-lik
36	160	86.5	34	6	ABU09803	Abu09803	HIV envel
37	160	86.5	34	6	ABB82817	Abb82817	C34 pepti
38	160	86.5	34	6	ABB82824	Abb82824	C34 pepti
39	160	86.5	34	6	ABB82823	Abb82823	C34 pepti
40	160	86.5	34	7	ADC07734	Adc07734	Human imm
41	160	86.5	34	8	ADF94455	Adf94455	Structure
42	160	86.5	34	8	ADO44129	Ado44129	Amino aci
43	160	86.5	34	8	ADN46048	Adn46048	C-helical
44	160	86.5	34	8	ADT77094	Adt77094	Antiviral
45	160	86.5	34	8	ADT76282	Adt76282	Antiviral

ALIGNMENTS

RESULT 1

ADO44134

ID ADO44134 standard; peptide; 34 AA.

XX

AC ADO44134;

XX

DT 15-JUL-2004 (first entry)

XX

DE Amino acid sequence of HIV variant gp41 peptide FB006M.

XX

KW gp41; HIV; antiviral; virostatic; antifusogenic; viral infection.

XX

OS Human immunodeficiency virus.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

SCORE Search Results Details for Application 10667966 and Search Result us-10-667-966b-11.rag.

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OM protein - protein search, using sw model

Run on: September 28, 2006, 04:38:19 ; Search time 81.0286 Seconds
(without alignments)
197.493 Million cell updates/sec

Title: US-10-667-966B-11
Perfect score: 184
Sequence: 1 WEEWDREINNYTELIHELIEESQNQQEKNEQELLX 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description

1	184	100.0	35	8	ADO44135	Ado44135	Amino aci
2	184	100.0	44	8	ADO44125	Ado44125	Amino aci
3	184	100.0	45	8	ADO44133	Ado44133	Amino aci
4	180	97.8	34	8	ADO44126	Ado44126	Amino aci
5	178	96.7	44	8	ADO44132	Ado44132	Amino aci
6	176	95.7	34	8	ADO44131	Ado44131	Amino aci
7	176	95.7	35	8	ADO44139	Ado44139	Amino aci
8	174	94.6	34	8	ADO44138	Ado44138	Amino aci
9	171	92.9	34	8	ADO44134	Ado44134	Amino aci
10	169	91.8	35	8	ADT76688	Adt76688	Antiviral
11	169	91.8	35	8	ADT76692	Adt76692	Antiviral
12	169	91.8	36	4	ABB02297	Abb02297	Viral cor
13	169	91.8	36	4	ABB02285	Abb02285	Viral cor
14	168	91.3	34	6	ABB82818	Abb82818	C34 pepti
15	168	91.3	34	6	ABR58073	Abr58073	HIV gp41
16	168	91.3	34	8	ADU66496	Adu66496	HIV-1 gp4
17	168	91.3	34	9	AED86966	Aed86966	C34 analo
18	168	91.3	34	9	AED86991	Aed86991	C34 analo
19	168	91.3	36	3	AAy89415	Aay89415	Core poly
20	168	91.3	36	3	AAy89401	Aay89401	Core poly
21	168	91.3	36	4	AAB77816	Aab77816	Core poly
22	168	91.3	36	4	AAU13369	Aau13369	DP178-lik
23	168	91.3	36	4	AAU13355	Aau13355	DP178-lik
24	168	91.3	344	8	ADR19628	Adr19628	Human imm
25	167	90.8	34	3	AAy89397	Aay89397	Core poly
26	167	90.8	34	3	AAy76979	Aay76979	HIV-1 gp4
27	167	90.8	34	3	AAB14534	Aab14534	HIV-1 iso
28	167	90.8	34	4	AAG63862	Aag63862	Amino aci
29	167	90.8	34	4	AAB85202	Aab85202	HIV gp41
30	167	90.8	34	4	AAB85203	Aab85203	HIV HXB3
31	167	90.8	34	4	AAB77798	Aab77798	Core poly
32	167	90.8	34	4	AAU70194	Aau70194	HIV viral
33	167	90.8	34	4	AAB99722	Aab99722	HIV-1 LAI
34	167	90.8	34	4	ABB00805	Abb00805	Viral DP1
35	167	90.8	34	4	ABB02281	Abb02281	Viral cor
36	167	90.8	34	4	AAB49501	Aab49501	C34 pepti
37	167	90.8	34	4	AAU13351	Aau13351	DP178-lik
38	167	90.8	34	6	ABU09803	Abu09803	HIV envel
39	167	90.8	34	6	ABB82817	Abb82817	C34 pepti
40	167	90.8	34	6	ABB82824	Abb82824	C34 pepti
41	167	90.8	34	6	ABB82823	Abb82823	C34 pepti
42	167	90.8	34	7	ADC07734	Adc07734	Human imm
43	167	90.8	34	8	ADF94455	Adf94455	Structure
44	167	90.8	34	8	ADO44129	Ado44129	Amino aci
45	167	90.8	34	8	ADN46048	Adn46048	C-helical

ALIGNMENTS

RESULT 1

ADO44135

ID ADO44135 standard; peptide; 35 AA.

XX

AC ADO44135;

XX

DT 15-JUL-2004 (first entry)

XX

DE Amino acid sequence of HIV variant gp41 peptide FB007M.

XX

KW gp41; HIV; antiviral; virostatic; antifusogenic; viral infection.

XX

OS Human immunodeficiency virus.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

SCORE Search Results Details for Application 10667966 and Search Result us-10-667-966b-13.rag.

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OM protein - protein search, using sw model

Run on: September 28, 2006, 04:38:19 ; Search time 92.6042 Seconds
(without alignments)
197.493 Million cell updates/sec

Title: US-10-667-966B-13
Perfect score: 219
Sequence: 1 WQEWEQKITALIEQAQIQQEKNEYELQKLDKWASLWEWFX 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description

1	219	100.0	40	8	ADO44137	Ado44137	Amino aci
2	217	99.1	39	3	AAy88648	Aay88648	Hybrid po
3	217	99.1	39	3	AAy89791	Aay89791	Core poly
4	217	99.1	39	3	AAy89790	Aay89790	Core poly
5	217	99.1	39	4	AAU06202	Aau06202	T1249 ant
6	217	99.1	39	4	AAB68862	Aab68862	Core poly
7	217	99.1	39	4	AAB78191	Aab78191	Core poly
8	217	99.1	39	4	AAB78088	Aab78088	Core poly
9	217	99.1	39	4	AAB78192	Aab78192	Core poly
10	217	99.1	39	4	ABB01198	Abb01198	Viral DP1
11	217	99.1	39	4	ABB02648	Abb02648	Viral cor
12	217	99.1	39	4	ABB02783	Abb02783	Viral cor
13	217	99.1	39	4	ABB01095	Abb01095	Viral DP1
14	217	99.1	39	4	ABB02544	Abb02544	Viral cor
15	217	99.1	39	4	ABB02647	Abb02647	Viral cor
16	217	99.1	39	4	ABB01199	Abb01199	Viral DP1
17	217	99.1	39	4	AAU13641	Aau13641	DP178-lik
18	217	99.1	39	4	AAU13745	Aau13745	DP178-lik
19	217	99.1	39	4	AAU13744	Aau13744	DP178-lik
20	217	99.1	39	4	AAB82966	Aab82966	Anti-HIV
21	217	99.1	39	5	AAE22296	Aae22296	gp41 fusi
22	217	99.1	39	5	ADE02667	Ade02667	Hybrid po
23	217	99.1	39	5	ADE02564	Ade02564	Hybrid po
24	217	99.1	39	5	ADE02803	Ade02803	Hybrid po
25	217	99.1	39	5	ADE02668	Ade02668	Hybrid po
26	217	99.1	39	6	AAE36031	Aae36031	HIV-1 gp4
27	217	99.1	39	7	ADC16751	Adc16751	HIV fusio
28	217	99.1	39	7	ADF16093	Adf16093	Human alb
29	217	99.1	39	7	ADF16088	Adf16088	Human alb
30	217	99.1	39	7	ADF16666	Adf16666	Human alb
31	217	99.1	39	8	ADN06890	Adn06890	Peptide T
32	217	99.1	39	8	ADO19045	Ado19045	T1249 pep
33	217	99.1	39	8	ADO44127	Ado44127	Amino aci
34	217	99.1	39	8	ADO43147	Ado43147	HIV-1 ant
35	217	99.1	39	8	ADS87225	Ads87225	HIV-1 gp4
36	217	99.1	39	8	ADU49738	Adu49738	Amino aci
37	217	99.1	39	8	ADU80540	Adu80540	Prior art
38	217	99.1	39	9	ADV95963	Adv95963	Inhibitor
39	217	99.1	39	9	ADV67533	Adv67533	Amino aci
40	217	99.1	39	9	ADZ40298	Adz40298	HIV-1 tra
41	217	99.1	39	9	AEA89544	Aea89544	HIV and S
42	217	99.1	39	9	AED15117	Aed15117	HIV entry
43	217	99.1	39	9	AED69158	Aed69158	HIV gp41
44	217	99.1	40	9	AED86990	Aed86990	T1249 ana
45	217	99.1	42	6	AAE36040	Aae36040	Cleavage

ALIGNMENTS

RESULT 1

ADO44137

ID ADO44137 standard; peptide; 40 AA.

XX

AC ADO44137;

XX

DT 15-JUL-2004 (first entry)

XX

DE Amino acid sequence of HIV variant gp41 peptide FB010KM.

XX

KW gp41; HIV; antiviral; virostatic; antifusogenic; viral infection.

XX

OS Human immunodeficiency virus.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

1	184	100.0	34	8	ADO44131	Ado44131	Amino aci
2	184	100.0	35	8	ADO44139	Ado44139	Amino aci
3	180	97.8	34	8	ADO44126	Ado44126	Amino aci
4	178	96.7	34	8	ADO44138	Ado44138	Amino aci
5	176	95.7	35	8	ADO44135	Ado44135	Amino aci
6	176	95.7	44	8	ADO44125	Ado44125	Amino aci
7	176	95.7	45	8	ADO44133	Ado44133	Amino aci
8	174	94.6	44	8	ADO44132	Ado44132	Amino aci
9	168	91.3	34	6	ABB82818	Abb82818	C34 pepti
10	168	91.3	34	9	AED86966	Aed86966	C34 analo
11	168	91.3	34	9	AED86991	Aed86991	C34 analo
12	167	90.8	34	8	ADO44134	Ado44134	Amino aci
13	167	90.8	35	8	ADT76532	Adt76532	Antiviral
14	167	90.8	35	8	ADT76539	Adt76539	Antiviral
15	165	89.7	35	8	ADT76688	Adt76688	Antiviral
16	165	89.7	35	8	ADT76692	Adt76692	Antiviral
17	165	89.7	36	4	ABB02297	Abb02297	Viral cor
18	165	89.7	36	4	ABB02285	Abb02285	Viral cor
19	165	89.7	36	8	ADS87334	Ads87334	HIV-1 gp4
20	164	89.1	34	6	ABR58073	Abr58073	HIV gp41
21	164	89.1	34	8	ADU66496	Adu66496	HIV-1 gp4
22	164	89.1	36	3	AAy89415	Aay89415	Core poly
23	164	89.1	36	3	AAy89401	Aay89401	Core poly
24	164	89.1	36	4	AAB77816	Aab77816	Core poly
25	164	89.1	36	4	AAU13369	Aaul3369	DP178-lik
26	164	89.1	36	4	AAU13355	Aaul3355	DP178-lik
27	164	89.1	344	8	ADR19628	Adr19628	Human imm
28	163	88.6	34	3	AAy89397	Aay89397	Core poly
29	163	88.6	34	3	AAy76979	Aay76979	HIV-1 gp4
30	163	88.6	34	3	AAB14534	Aab14534	HIV-1 iso
31	163	88.6	34	4	AAG63862	Aag63862	Amino aci
32	163	88.6	34	4	AAB85202	Aab85202	HIV gp41
33	163	88.6	34	4	AAB85203	Aab85203	HIV HXB3
34	163	88.6	34	4	AAB77798	Aab77798	Core poly
35	163	88.6	34	4	AAU70194	Aau70194	HIV viral
36	163	88.6	34	4	AAB99722	Aab99722	HIV-1 LAI
37	163	88.6	34	4	ABB00805	Abb00805	Viral DP1
38	163	88.6	34	4	ABB02281	Abb02281	Viral cor
39	163	88.6	34	4	AAB49501	Aab49501	C34 pepti
40	163	88.6	34	4	AAU13351	Aau13351	DP178-lik
41	163	88.6	34	6	ABU09803	Abu09803	HIV envel
42	163	88.6	34	6	ABB82817	Abb82817	C34 pepti
43	163	88.6	34	6	ABB82824	Abb82824	C34 pepti
44	163	88.6	34	6	ABB82823	Abb82823	C34 pepti
45	163	88.6	34	7	ADC07734	Adc07734	Human imm

ALIGNMENTS

RESULT 1

ADO44131

ID ADO44131 standard; peptide; 34 AA.

XX

AC ADO44131;

XX

DT 15-JUL-2004 (first entry)

XX

DE Amino acid sequence of HIV variant gp41 peptide FB066.

XX

KW gp41; HIV; antiviral; virostatic; antifusogenic; viral infection.

XX

OS Human immunodeficiency virus.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

RESULT 1

AA88648

ID AAY88648 standard; peptide; 39 AA.

XX

AC AAY88648;

XX

DT 06-AUG-2003 (revised)

DT 23-MAY-2000 (first entry)

XX

DE Hybrid polypeptide fragment.

XX

KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;

KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;

KW anti-fusogenic; differentiation factor; interleukin; interferon;

KW colony stimulating factor; hormone; angiogenic factor.

XX

OS Retroviridae.

OS Synthetic.

XX

PN WO9959615-A1.

XX

PD 25-NOV-1999.

XX

PF 20-MAY-1999; 99WO-US011219.

XX

PR 20-MAY-1998; 98US-00082279.

XX

PA (TRIM-) TRIMERIS INC.

XX

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX

DR WPI; 2000-136792/12.

XX

PT A new hybrid polypeptide with enhanced pharmacokinetic properties

PT comprises enhancer sequence.

XX

PS Claim 14; Page 95; 124pp; English.

XX

CC The invention relates to hybrid polypeptides comprising enhancer peptide

CC sequence linked to core polypeptides. The enhancer polypeptides are

CC derived from various retroviral envelope (gp41) protein sequences,

CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the

CC pharmacokinetic properties such as increasing the half-life of any core

CC polypeptide that they are linked to. The core polypeptides are any

CC polypeptide that may be introduced into a living system and that can

CC function as a pharmacologically useful peptide for the treatment or

CC prevention of a disease. The core polypeptides are bioactive peptides

CC selected from a growth factor, cytokine, differentiation factor,

CC interleukin, interferon, colony stimulating factor, hormone or angiogenic

CC factor. The peptides of the invention can be used for inhibiting viral

CC infection and can be used in anti-viral and anti-fusogenic treatments.

CC Sequences AAY88648-Y88650 represent specific examples of hybrid

CC polypeptides. (Updated on 06-AUG-2003 to correct OS field.)

XX

SQ Sequence 39 AA;

Query Match 100.0%; Score 219; DB 3; Length 39;

Best Local Similarity 100.0%; Pred. No. 4.8e-19;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WQWEQKITALLEQAQIQQEKNEYELQKLDKWASLWEWF 39

|||||

Db 1 WQWEQKITALLEQAQIQQEKNEYELQKLDKWASLWEWF 39

1	239	100.0	44	8	ADO44125	Ado44125	Amino aci
2	239	100.0	45	8	ADO44133	Ado44133	Amino aci
3	233	97.5	44	8	ADO44132	Ado44132	Amino aci
4	222	92.9	51	9	AEB96643	Aeb96643	HIV gp41
5	222	92.9	52	9	AEB96642	Aeb96642	HIV gp41
6	222	92.9	53	9	AEB96641	Aeb96641	HIV gp41
7	222	92.9	54	9	AEB96640	Aeb96640	HIV gp41
8	222	92.9	55	9	AEB96639	Aeb96639	HIV gp41
9	222	92.9	56	9	AEB96638	Aeb96638	HIV gp41
10	222	92.9	57	5	AAO18796	Aao18796	HIV gp41
11	222	92.9	57	9	ADY71517	Ady71517	HIV-1 tra
12	222	92.9	57	9	AEB96637	Aeb96637	HIV gp41
13	222	92.9	58	4	AAU14128	Aau14128	DPI78-lik
14	222	92.9	58	9	AEB96636	Aeb96636	HIV gp41
15	222	92.9	59	9	AEB96635	Aeb96635	HIV gp41
16	222	92.9	60	9	AEB96634	Aeb96634	HIV gp41
17	222	92.9	61	9	AEB96633	Aeb96633	HIV gp41
18	222	92.9	62	9	AEB96632	Aeb96632	HIV gp41
19	222	92.9	63	9	AEB96631	Aeb96631	HIV gp41
20	222	92.9	64	8	ADN06887	Adn06887	Human imm
21	222	92.9	64	8	ADS87222	Ads87222	HIV-1 gp4
22	222	92.9	64	9	AEB32178	Aeb32178	HIV glyco
23	222	92.9	64	9	AEB96630	Aeb96630	HIV gp41
24	222	92.9	64	9	AED69064	Aed69064	HIV gp41
25	222	92.9	65	9	AEB96629	Aeb96629	HIV gp41
26	222	92.9	66	9	AEB96628	Aeb96628	HIV gp41
27	222	92.9	66	9	AEB96670	Aeb96670	HIV gp41
28	222	92.9	67	9	AEB96627	Aeb96627	HIV gp41
29	222	92.9	67	9	AEB96669	Aeb96669	HIV gp41
30	222	92.9	68	9	AEB96668	Aeb96668	HIV gp41
31	222	92.9	69	9	AEB96626	Aeb96626	HIV gp41
32	222	92.9	69	9	AEB96667	Aeb96667	HIV gp41
33	222	92.9	70	9	AEB96625	Aeb96625	HIV gp41
34	222	92.9	70	9	AEB96666	Aeb96666	HIV gp41
35	222	92.9	71	9	AEB96665	Aeb96665	HIV gp41
36	222	92.9	71	9	AEB96624	Aeb96624	HIV gp41
37	222	92.9	72	9	AEB96664	Aeb96664	HIV gp41
38	222	92.9	72	9	AEB96623	Aeb96623	HIV gp41
39	222	92.9	73	9	AEB96554	Aeb96554	HIV gp41
40	222	92.9	73	9	AEB96549	Aeb96549	HIV gp41
41	222	92.9	73	9	AEB96622	Aeb96622	HIV gp41
42	222	92.9	114	2	AAR77185	Aar77185	Chimeric
43	222	92.9	138	3	AAY69792	Aay69792	HIV-1 gp4
44	222	92.9	138	8	ADO10354	Ado10354	HIV1 glyc
45	222	92.9	140	1	AAP93342	Aap93342	HIV-1 env

ALIGNMENTS

RESULT 1

ADO44125

ID ADO44125 standard; peptide; 44 AA.

XX

AC ADO44125;

XX

DT 15-JUL-2004 (first entry)

XX

DE Amino acid sequence of HIV variant gp41 peptide FB005.

XX

KW gp41; HIV; antiviral; virostatic; antifusogenic; viral infection.

XX

OS Human immunodeficiency virus.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

SCORE Search Results Details for Application 10667966 and Search Result us-10-667-966b-2.rag.

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OM protein - protein search, using sw model

Run on: September 28, 2006, 04:38:19 ; Search time 78.7135 Seconds
(without alignments)
197.493 Million cell updates/sec

Title: US-10-667-966B-2
Perfect score: 184
Sequence: 1 WEEWDREINNYTKLIHELIEESQNQQEKNEQELL 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	%
No.	Score Match Length DB ID	Description

1	184	100.0	34	8	ADO44126	Ado44126	Amino aci
2	180	97.8	34	8	ADO44131	Ado44131	Amino aci
3	180	97.8	35	8	ADO44139	Ado44139	Amino aci
4	180	97.8	35	8	ADO44135	Ado44135	Amino aci
5	180	97.8	44	8	ADO44125	Ado44125	Amino aci
6	180	97.8	45	8	ADO44133	Ado44133	Amino aci
7	178	96.7	44	8	ADO44132	Ado44132	Amino aci
8	174	94.6	34	8	ADO44138	Ado44138	Amino aci
9	172	93.5	34	6	ABB82818	Abb82818	C34 pepti
10	172	93.5	34	9	AED86966	Aed86966	C34 analo
11	172	93.5	34	9	AED86991	Aed86991	C34 analo
12	171	92.9	34	8	ADO44134	Ado44134	Amino aci
13	169	91.8	35	8	ADT76688	Adt76688	Antiviral
14	169	91.8	35	8	ADT76692	Adt76692	Antiviral
15	169	91.8	36	4	ABB02297	Abb02297	Viral cor
16	169	91.8	36	4	ABB02285	Abb02285	Viral cor
17	168	91.3	34	6	ABR58073	Abr58073	HIV gp41
18	168	91.3	34	8	ADU66496	Adu66496	HIV-1 gp4
19	168	91.3	36	3	AAY89415	Aay89415	Core poly
20	168	91.3	36	3	AAY89401	Aay89401	Core poly
21	168	91.3	36	4	AAB77816	Aab77816	Core poly
22	168	91.3	36	4	AAU13369	Aau13369	DP178-lik
23	168	91.3	36	4	AAU13355	Aau13355	DP178-lik
24	168	91.3	344	8	ADR19628	Adr19628	Human imm
25	167	90.8	34	3	AAY89397	Aay89397	Core poly
26	167	90.8	34	3	AAY76979	Aay76979	HIV-1 gp4
27	167	90.8	34	3	AAB14534	Aab14534	HIV-1 iso
28	167	90.8	34	4	AAG63862	Aag63862	Amino aci
29	167	90.8	34	4	AAB85202	Aab85202	HIV gp41
30	167	90.8	34	4	AAB85203	Aab85203	HIV HXB3
31	167	90.8	34	4	AAB77798	Aab77798	Core poly
32	167	90.8	34	4	AAU70194	Aau70194	HIV viral
33	167	90.8	34	4	AAB99722	Aab99722	HIV-1 LAI
34	167	90.8	34	4	ABB00805	Abb00805	Viral DP1
35	167	90.8	34	4	ABB02281	Abb02281	Viral cor
36	167	90.8	34	4	AAB49501	Aab49501	C34 pepti
37	167	90.8	34	4	AAU13351	Aau13351	DP178-lik
38	167	90.8	34	6	ABU09803	Abu09803	HIV envel
39	167	90.8	34	6	ABB82817	Abb82817	C34 pepti
40	167	90.8	34	6	ABB82824	Abb82824	C34 pepti
41	167	90.8	34	6	ABB82823	Abb82823	C34 pepti
42	167	90.8	34	7	ADC07734	Adc07734	Human imm
43	167	90.8	34	8	ADF94455	Adf94455	Structure
44	167	90.8	34	8	ADO44129	Ado44129	Amino aci
45	167	90.8	34	8	ADN46048	Adn46048	C-helical

ALIGNMENTS

RESULT 1

ADO44126

ID ADO44126 standard; peptide; 34 AA.

XX

AC ADO44126;

XX

DT 15-JUL-2004 (first entry)

XX

DE Amino acid sequence of HIV variant gp41 peptide FB006.

XX

KW gp41; HIV; antiviral; virostatic; antifusogenic; viral infection.

XX

OS Human immunodeficiency virus.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

SCORE Search Results Details for Application 10667966 and Search Result us-10-667-966b-3.rag.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
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OM protein - protein search, using sw model

Run on: September 28, 2006, 04:38:19 ; Search time 90.2891.Seconds
(without alignments)
197.493 Million cell updates/sec

Title: US-10-667-966B-3
Perfect score: 219
Sequence: 1 WQEWQKITALLEQAQIQQEKNEYELQKLDKWASLWEWF 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	%
No.	Score Match Length DB ID	Description

1	219	100.0	39	3	AAy88648	Aay88648 Hybrid po
2	219	100.0	39	3	AAy89791	Aay89791 Core poly
3	219	100.0	39	3	AAy89790	Aay89790 Core poly
4	219	100.0	39	4	AAU06202	Aau06202 T1249 ant
5	219	100.0	39	4	AAB68862	Aab68862 Core poly
6	219	100.0	39	4	AAB78191	Aab78191 Core poly
7	219	100.0	39	4	AAB78088	Aab78088 Core poly
8	219	100.0	39	4	AAB78192	Aab78192 Core poly
9	219	100.0	39	4	ABB01198	Abb01198 Viral DP1
10	219	100.0	39	4	ABB02648	Abb02648 Viral cor
11	219	100.0	39	4	ABB02783	Abb02783 Viral cor
12	219	100.0	39	4	ABB01095	Abb01095 Viral DP1
13	219	100.0	39	4	ABB02544	Abb02544 Viral cor
14	219	100.0	39	4	ABB02647	Abb02647 Viral cor
15	219	100.0	39	4	ABB01199	Abb01199 Viral DP1
16	219	100.0	39	4	AAU13641	Aau13641 DP178-lik
17	219	100.0	39	4	AAU13745	Aau13745 DP178-lik
18	219	100.0	39	4	AAU13744	Aau13744 DP178-lik
19	219	100.0	39	4	AAB82966	Aab82966 Anti-HIV
20	219	100.0	39	5	AAE22296	Aae22296 gp41 fusi
21	219	100.0	39	5	ADE02667	Ade02667 Hybrid po
22	219	100.0	39	5	ADE02564	Ade02564 Hybrid po
23	219	100.0	39	5	ADE02803	Ade02803 Hybrid po
24	219	100.0	39	5	ADE02668	Ade02668 Hybrid po
25	219	100.0	39	6	AAE36031	Aae36031 HIV-1 gp4
26	219	100.0	39	7	ADC16751	Adc16751 HIV fusio
27	219	100.0	39	7	ADF16093	Adf16093 Human alb
28	219	100.0	39	7	ADF16088	Adf16088 Human alb
29	219	100.0	39	7	ADF16666	Adf16666 Human alb
30	219	100.0	39	8	ADN06890	Adn06890 Peptide T
31	219	100.0	39	8	ADO19045	Ado19045 T1249 pep
32	219	100.0	39	8	ADO44127	Ado44127 Amino aci
33	219	100.0	39	8	ADO43147	Ado43147 HIV-1 ant
34	219	100.0	39	8	ADS87225	Ads87225 HIV-1 gp4
35	219	100.0	39	8	ADU49738	Adu49738 Amino aci
36	219	100.0	39	8	ADU80540	Adu80540 Prior art
37	219	100.0	39	9	ADV95963	Adv95963 Inhibitor
38	219	100.0	39	9	ADV67533	Adv67533 Amino aci
39	219	100.0	39	9	ADZ40298	Adz40298 HIV-1 tra
40	219	100.0	39	9	AEA89544	Aea89544 HIV and S
41	219	100.0	39	9	AED15117	Aed15117 HIV entry
42	219	100.0	39	9	AED69158	Aed69158 HIV gp41
43	219	100.0	40	9	AED86990	Aed86990 T1249 ana
44	219	100.0	42	6	AAE36040	Aae36040 Cleavage
45	219	100.0	51	6	AAE36038	Aae36038 M-HHHHHH-

ALIGNMENTS

RESULT 1

AAy88648

ID AAY88648 standard; peptide; 39 AA..

XX

AC AAY88648;

XX

DT 06-AUG-2003 (revised)

DT 23-MAY-2000 (first entry)

XX

DE Hybrid polypeptide fragment.

XX

KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;

KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;

KW anti-fusogenic; differentiation factor; interleukin; interferon;

KW colony stimulating factor; hormone; angiogenic factor.

XX

OS Retroviridae.

SCORE Search Results Details for Application 10667966 and Search Result us-10-667-966b-7.rag.

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions
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OM protein - protein search, using sw model

Run on: September 28, 2006, 04:38:19 ; Search time 78.7135 Seconds
(without alignments)
197.493 Million cell updates/sec

Title: US-10-667-966B-7
Perfect score: 184
Sequence: 1 WEEWDREINNYTKLIHELIEESQNQQEENEQELL 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description

1	184	100.0	34	8	ADO44131	Ado44131	Amino aci
2	184	100.0	35	8	ADO44139	Ado44139	Amino aci
3	180	97.8	34	8	ADO44126	Ado44126	Amino aci
4	178	96.7	34	8	ADO44138	Ado44138	Amino aci
5	176	95.7	35	8	ADO44135	Ado44135	Amino aci
6	176	95.7	44	8	ADO44125	Ado44125	Amino aci
7	176	95.7	45	8	ADO44133	Ado44133	Amino aci
8	174	94.6	44	8	ADO44132	Ado44132	Amino aci
9	168	91.3	34	6	ABB82818	Abb82818	C34 pepti
10	168	91.3	34	9	AED86966	Aed86966	C34 analo
11	168	91.3	34	9	AED86991	Aed86991	C34 analo
12	167	90.8	34	8	ADO44134	Ado44134	Amino aci
13	167	90.8	35	8	ADT76532	Adt76532	Antiviral
14	167	90.8	35	8	ADT76539	Adt76539	Antiviral
15	165	89.7	35	8	ADT76688	Adt76688	Antiviral
16	165	89.7	35	8	ADT76692	Adt76692	Antiviral
17	165	89.7	36	4	ABB02297	Abb02297	Viral cor
18	165	89.7	36	4	ABB02285	Abb02285	Viral cor
19	165	89.7	36	8	ADS87334	Ads87334	HIV-1 gp4
20	164	89.1	34	6	ABR58073	Abr58073	HIV gp41
21	164	89.1	34	8	ADU66496	Adu66496	HIV-1 gp4
22	164	89.1	36	3	AAy89415	Aay89415	Core poly
23	164	89.1	36	3	AAy89401	Aay89401	Core poly
24	164	89.1	36	4	AAB77816	Aab77816	Core poly
25	164	89.1	36	4	AAU13369	Aau13369	DP178-lik
26	164	89.1	36	4	AAU13355	Aau13355	DP178-lik
27	164	89.1	344	8	ADR19628	Adr19628	Human imm
28	163	88.6	34	3	AAy89397	Aay89397	Core poly
29	163	88.6	34	3	AAy76979	Aay76979	HIV-1 gp4
30	163	88.6	34	3	AAB14534	Aab14534	HIV-1 iso
31	163	88.6	34	4	AAG63862	Aag63862	Amino aci
32	163	88.6	34	4	AAB85202	Aab85202	HIV gp41
33	163	88.6	34	4	AAB85203	Aab85203	HIV HXB3
34	163	88.6	34	4	AAB77798	Aab77798	Core poly
35	163	88.6	34	4	AAU70194	Aau70194	HIV viral
36	163	88.6	34	4	AAB99722	Aab99722	HIV-1 LAI
37	163	88.6	34	4	ABB00805	Abb00805	Viral DP1
38	163	88.6	34	4	ABB02281	Abb02281	Viral cor
39	163	88.6	34	4	AAB49501	Aab49501	C34 pepti
40	163	88.6	34	4	AAU13351	Aau13351	DP178-lik
41	163	88.6	34	6	ABU09803	Abu09803	HIV envel
42	163	88.6	34	6	ABB82817	Abb82817	C34 pepti
43	163	88.6	34	6	ABB82824	Abb82824	C34 pepti
44	163	88.6	34	6	ABB82823	Abb82823	C34 pepti
45	163	88.6	34	7	ADC07734	Adc07734	Human imm

ALIGNMENTS

RESULT 1

ADO44131

ID ADO44131 standard; peptide; 34 AA.

XX

AC ADO44131;

XX

DT 15-JUL-2004 (first entry)

XX

DE Amino acid sequence of HIV variant gp41 peptide FB066.

XX

KW gp41; HIV; antiviral; virostatic; antifusogenic; viral infection.

XX

OS Human immunodeficiency virus.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

SCORE Search Results Details for Application 10667966 and Search Result us-10-667-966b-8.rag.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10667966 and Search Result us-10-667-966b-8.rag.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 28, 2006, 04:38:19 ; Search time 101.865 Seconds
(without alignments)
197.493 Million cell updates/sec

Title: US-10-667-966B-8
Perfect score: 234
Sequence: 1 SLEQIWNNMTWEEWDREINN.....IHELIEESQNQQEKNEQELL 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description

1	233	99.6	44	8	ADO44132	Ado44132 Amino aci
2	233	99.6	44	8	ADO44125	Ado44125 Amino aci
3	233	99.6	45	8	ADO44133	Ado44133 Amino aci
4	222	94.9	51	9	AEB96643	Aeb96643 HIV gp41
5	222	94.9	52	9	AEB96642	Aeb96642 HIV gp41
6	222	94.9	53	9	AEB96641	Aeb96641 HIV gp41
7	222	94.9	54	9	AEB96640	Aeb96640 HIV gp41
8	222	94.9	55	9	AEB96639	Aeb96639 HIV gp41
9	222	94.9	56	9	AEB96638	Aeb96638 HIV gp41
10	222	94.9	57	5	AAO18796	Aao18796 HIV gp41
11	222	94.9	57	9	ADY71517	Ady71517 HIV-1 tra
12	222	94.9	57	9	AEB96637	Aeb96637 HIV gp41
13	222	94.9	58	4	AAU14128	Aaul14128 DP178-lik
14	222	94.9	58	9	AEB96636	Aeb96636 HIV gp41
15	222	94.9	59	9	AEB96635	Aeb96635 HIV gp41
16	222	94.9	60	9	AEB96634	Aeb96634 HIV gp41
17	222	94.9	61	9	AEB96633	Aeb96633 HIV gp41
18	222	94.9	62	9	AEB96632	Aeb96632 HIV gp41
19	222	94.9	63	9	AEB96631	Aeb96631 HIV gp41
20	222	94.9	64	8	ADN06887	Adn06887 Human imm
21	222	94.9	64	8	ADS87222	Ads87222 HIV-1 gp4
22	222	94.9	64	9	AEB32178	Aeb32178 HIV glyco
23	222	94.9	64	9	AEB96630	Aeb96630 HIV gp41
24	222	94.9	64	9	AED69064	Aed69064 HIV gp41
25	222	94.9	65	9	AEB96629	Aeb96629 HIV gp41
26	222	94.9	66	9	AEB96628	Aeb96628 HIV gp41
27	222	94.9	66	9	AEB96670	Aeb96670 HIV gp41
28	222	94.9	67	9	AEB96627	Aeb96627 HIV gp41
29	222	94.9	67	9	AEB96669	Aeb96669 HIV gp41
30	222	94.9	68	9	AEB96668	Aeb96668 HIV gp41
31	222	94.9	69	9	AEB96626	Aeb96626 HIV gp41
32	222	94.9	69	9	AEB96667	Aeb96667 HIV gp41
33	222	94.9	70	9	AEB96625	Aeb96625 HIV gp41
34	222	94.9	70	9	AEB96666	Aeb96666 HIV gp41
35	222	94.9	71	9	AEB96665	Aeb96665 HIV gp41
36	222	94.9	71	9	AEB96624	Aeb96624 HIV gp41
37	222	94.9	72	9	AEB96664	Aeb96664 HIV gp41
38	222	94.9	72	9	AEB96623	Aeb96623 HIV gp41
39	222	94.9	73	9	AEB96554	Aeb96554 HIV gp41
40	222	94.9	73	9	AEB96549	Aeb96549 HIV gp41
41	222	94.9	73	9	AEB96622	Aeb96622 HIV gp41
42	222	94.9	114	2	AAR77185	Aar77185 Chimeric
43	222	94.9	138	3	AAY69792	Aay69792 HIV-1 gp4
44	222	94.9	138	8	ADO10354	Ado10354 HIV1 glyc
45	222	94.9	140	1	AAP93342	Aap93342 HIV-1 env

ALIGNMENTS

RESULT 1

ADO44132

ID ADO44132 standard; peptide; 44 AA.

XX

AC ADO44132;

XX

DT 15-JUL-2004 (first entry)

XX

DE Amino acid sequence of HIV variant gp41 peptide FB005M.

XX

KW gp41; HIV; antiviral; virostatic; antifusogenic; viral infection.

XX

OS Human immunodeficiency virus.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1